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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/981,353	10/11/2001	Amy W. Lasek	PA-0038 US	6892

27904 7590 08/12/2003

INCYTE CORPORATION (formerly known as Incyte Genomics, Inc.)
3160 PORTER DRIVE
PALO ALTO, CA 94304

EXAMINER
MARTINELL, JAMES

ART UNIT	PAPER NUMBER
1631	10

DATE MAILED: 08/12/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/981,353	LASEK ET AL.	
	Examiner	Art Unit	
	James Martinell	1631	

-- The MAILING DATE of this communication appears on th cover she t with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *02 June 2003* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-20* is/are pending in the application.

4a) Of the above claim(s) *2 and 13-20* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1 and 3-12* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *6* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

Applicant's election of Group I in Paper No. 9 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)). Applicants' response (paper no. 9) did not address the aspects of the requirement for restriction between Groups I and VI, VII, and VIII and so the election is treated as an election without traverse in connection with the independence and distinctness of Groups I and VI-VIII as outlined in the Office action mailed May 2, 2003. Applicants" arguments in connection with rejoining Groups I and II is not persuasive because Group II claims a combination of SEQ ID NOs that is different from the elected combination.

Claims 2 and 13-20 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in Paper No. 9.

Applicants' arguments in connection with rejoining claims 4-12 with Group I, claims 1 and 3, is persuasive. Thus, claims 4-12 are hereby rejoined with claims 1 and 3 to make up Group I. Claims 1 and 3-12 are examined in this Office action. The combination examined includes the combinations containing each one of SEQ ID NOs: 24, 47, 81, 104, 114, 165, and 172 (see paper no. 9, paragraph bridging pages 6-7). SEQ ID NOs: 24, 47, 81, 104, 114, 165, and 172 have been searched (see MPEP 803.04 (pages 800-10 and 11, August 2001 edition) in connection with USPTO search procedures for nucleotide sequence combination claims).

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1 and 3-8 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claims are vague, indefinite, incomplete, misdescriptive, and inaccurate.

(a) The recitation of "cDNAs that are differentially expressed" (claim 1) is inaccurate and misdescriptive because cDNAs are not expressed, but are artificial constructs (*e.g.*, see the definition in Lewin).

(b) Claim 1 is vague and indefinite because it includes more combinations than the elected combinations (*e.g.*, see paper no. 9, paragraph bridging pages 6-7).

(c) The recitation of "that disease" (claim 6) is incomplete because there is no antecedent basis for the term.

(d) The recitation of "specifically binds" (claim 7) is vague, indefinite, and incomplete because the term is a relative one and no frame of reference is given. The determination or characterization of specific binding requires knowledge or disclosure of other potential binding partners in the reaction mixture. None is given or mentioned; thus the claim is vague, indefinite, and incomplete.

(e) The recitation of "specific binding" (claim 7) is vague, indefinite, and incomplete for reasons given in (c) immediately above.

(f) The recitation of "mimetics" (claim 8) is vague and indefinite because it is not clear what is meant by the term.

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1 and 3-12 are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility. The instant application does not disclose a nexus between any particular or anticipated hybridization results to SEQ ID NOs: 24, 47, 81, 104, 114, 165, and 172 and any disease state or non-disease state. The hybridization data shown in Table 1 and discussed on pages 9-10 of the instant application are not results of actual gene expression because they are disclosed as being cDNAs that hybridize to an array. Since cDNAs are artificial constructs, they do not necessarily reflect levels of

expression of genes. In addition, SEQ ID NO 47 (Clone ID 1695477) is not expressed in polyp or tumor cells at half the level of that of normal cells as is stated in the application in the paragraph bridging pages 9-10 (average downregulation according to Table 1 (page 2 line 19) is -1.07). Likewise, SEQ ID NO: 104 (Clone ID 2132203 is downregulated by an average of -1.48 (Table 1, page 3, line 33) and SEQ ID NO: 114 (Clone ID 2513883) is downregulated by an average of -1.39 (Table 1, page 2, line 27). No data for SEQ ID NO: 172 (Clone ID 1846463) are seen in Table 1 at all. Finally, the application does not disclose how the cDNA measurements were made.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1 and 3-12 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. The discussion in the rejection under 35 USC § 101 hereinabove is incorporated here. In addition, claim 1 is not enabled in its full breadth for reciting "differentially expressed in a colon disorder" because the instant application does not enable diagnosis of any colon disorder.

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of the application for patent in the United States.

> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 9-12 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by either one of Hillman et al ((WO 99/41375 (August 19, 1999)) or Gunn et al (WO 98/38203 (September 3, 1998)). Hillman et al discloses a DNA that is 100% identical to SEQ ID NO: 81 of the instant application (see "Alignment Hillman" attached to this Office action). The abstract and pages 32-35 of Hillman et al teach the heterologous expression of the DNA. Thus, the claims embrace the polynucleotide, vectors, host cells, and method of making a polypeptide taught in Hillman et al. Gunn et al discloses a DNA that is 96.5% identical to SEQ ID NO: 172 of the instant application (see "Alignment Gunn" attached to this Office action). Page 10, lines 7-20 and page 21, line 24 through page 24, line 21 32-35 of Gunn et al teach the heterologous expression of the DNA. Thus, the claims embrace the polynucleotide, vectors, host cells, and method of making a polypeptide taught in Gunn et al.

Claims 9-12 are rejected under 35 U.S.C. 102(e) as being anticipated by Bandman et al (U.S. Patent No. 6,132,964).

The applied reference has a common assignee with the instant application. Based upon the earlier effective U.S. filing date of the reference, it constitutes prior art under 35 U.S.C. 102(e). This rejection under 35 U.S.C. 102(e) might be overcome either by a showing under 37 CFR 1.132 that any invention disclosed but not claimed in the reference was derived from the inventor of this application and is thus not the invention "by another," or by an appropriate showing under 37 CFR 1.131.

Claims 9-12 are directed to an invention not patentably distinct from claims 5-10 of commonly assigned U.S. Patent No. 6,132,964. Specifically, SEQ ID NO: 13 of U.S. Patent No. 6,132,964 is the same as SEQ ID NO: 47 of the instant claims.

Claims 9-12 are rejected under 35 U.S.C. 103(a) as being obvious over Bandman et al (U.S. Patent No. 6,132,964).

The applied reference has a common assignee with the instant application. Based upon the earlier effective U.S. filing date of the reference, it constitutes prior art only under 35 U.S.C. 102(e). This rejection under 35 U.S.C. 103(a) might be overcome by: (1) a showing under 37 CFR 1.132 that any invention disclosed but not claimed in the reference was derived from the inventor of this application and is thus not an invention "by another"; (2) a showing of a date of invention for the claimed subject matter of the application which corresponds to subject matter disclosed but not claimed in the reference, prior to the effective U.S. filing date of the reference under 37 CFR 1.131; or (3) an oath or declaration under 37 CFR 1.130 stating that the application and reference are currently owned by the same party and that the inventor named in the application is the prior inventor under 35 U.S.C. 104, together with a terminal disclaimer in accordance with 37 CFR 1.321(c). For applications filed on or after November 29, 1999, this rejection might also be overcome by showing that the subject matter of the reference and the claimed invention were, at the time the invention was made, owned by the same person or subject to an obligation of assignment to the same person. See MPEP § 706.02(l)(1) and § 706.02(l)(2). Bandman et al discloses a DNA (SEQ ID NO: 13) that is 100% identical to SEQ ID NO: 47 of the instant application (see "Alignment Bandman" attached to this Office action). Column 19, line 7 through column 22, line 38 of Bandman et al teach the heterologous expression of the DNA. Thus, the claims embrace the polynucleotide, vectors, host cells, and method of making a polypeptide taught in Bandman et al.

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Omum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 9-12 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 5-10 of U.S. Patent No. 6,132,964. Although the conflicting claims are not identical, they are not patentably distinct from each other because SEQ ID NO: 13 of U.S. Patent No. 6,132,964 is the same as SEQ ID NO: 47 of the instant claims.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to James Martinell whose telephone number is (703) 308-0296. The fax phone number for Examiner Martinell's desktop workstation is (703) 746-5162. The examiner works a flexible schedule and can be reached by phone and voice mail. Alternatively, a request for a return telephone call may be e-mailed to james.martinell@uspto.gov. Since e-mail communications may not be secure, it is suggested that information in such requests be limited to name, phone number, and the best time to return the call.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Michael Woodward, can be reached on (703) 305-4028.

Please take note of this new Official Fax Phone Number

The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

James Martinell, Ph.D.
Primary Examiner
Art Unit 1631

Alignment Hillman 1/2

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 03:41:41 ; Search time 224.967 Seconds
(without alignments)
13183.634 Million cell updates/sec

Title: US-09-981-353-81
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1317	100.0	1317	20	AAZ06368	Human receptor pro
2	1108	84.1	1141	21	AAZ95381	Human colon specif
3	1084.4	82.3	1291	21	AAA26287	Human secreted pro
4	1079	81.9	1292	21	AAA26331	Human secreted pro
5	712.8	54.1	854	23	AAS81191	DNA encoding novel
6	389.6	29.6	441	21	AAC98717	Human colon cancer
7	303.6	23.1	351	22	AAS37436	Novel human diagno
8	292.6	22.2	342	22	AAS37580	Novel human diagno
9	291.2	22.1	373	22	AAF66008	Novel human polynu
10	288.6	21.9	383	22	AAS37423	Novel human diagno
11	276	21.0	370	22	AAF65997	Novel human polynu
12	81.2	6.2	1236	19	AAV48114	Nucleotide sequenc
13	81.2	6.2	1336	21	AAZ51573	Human cell surface
14	81.2	6.2	1336	24	ABK39631	cDNA encoding L985
15	81.2	6.2	1374	21	AAC99077	Human pancreatic c
16	81.2	6.2	1375	24	ABL90599	Human polynucleoti
17	79.6	6.0	861	24	ABK39776	DNA encoding Ral2S
18	79.6	6.0	1155	24	ABK39775	DNA encoding Ral2-
19	79.6	6.0	1353	24	ABK39774	cDNA encoding lung
20	74.8	5.7	932	22	AAD19723	Dendritic cell (DC
21	74.8	5.7	945	19	AAV59668	Human secreted pro
22	74.8	5.7	1001	21	AAZ52580	Human secreted pro
23	74.8	5.7	1036	22	AAD19722	Dendritic cell (DC
24	74.8	5.7	1106	22	ABA09233	Human secreted pro
25	74.8	5.7	1106	22	AAH99750	Human protein enco
26	74.8	5.7	1108	22	AAF63724	Human hHAIERbs-iso
27	74.8	5.7	1289	22	AAH79291	Human cell surface
28	74.8	5.7	1488	20	AAZ33586	Human breast tumou
29	74.8	5.7	1522	20	AAZ06369	Human receptor pro
30	74.8	5.7	1570	21	AAA26426	Human secreted pro
31	74.8	5.7	1728	24	ABK34885	Human cDNA encodin
32	74.8	5.7	1743	21	AAF18295	Lung cancer associ
33	74.8	5.7	1871	22	AAH35024	Human colon cancer
34	74.8	5.7	1871	24	ABL90750	Human polynucleoti
35	74.8	5.7	2192	21	AAA27130	Human inflammation
36	74.4	5.6	648	24	ABQ58726	Human colon cancer
37	72	5.5	1060	20	AAX97730	Extended human sec
38	71.2	5.4	2545	11	AAQ04645	Encodes beta subun
39	71.2	5.4	2545	12	AAQ14734	Encodes beta subun
40	71.2	5.4	2545	14	AAQ51021	Human FceRI beta g
41	69.2	5.3	708	22	AAF77694	Murine wild-type F
42	61.2	4.6	999	22	AAH99112	Human EST-derived
43	61.2	4.6	1025	23	AAS76894	DNA encoding novel
44	60	4.6	60	24	ABN38453	Human spliced tran
c 45	60	4.6	489	24	ABL38455	Human colon tumour

ALIGNMENTS

RESULT 1
AAZ06368
ID AAZ06368 standard; DNA; 1317 BP.
XX
AC AAZ06368;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human receptor protein (HURP) 3 nucleotide sequence.
XX
KW receptor; cancer; autoimmune disorder; inflammation;
KW antagonist; cell surface protein; cell signalling;
KW antibody; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 221..1024
FT /*tag= a
FT /product= Human receptor protein 3
XX
PN WO9941375-A2.
XX
PD 19-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US02572.
XX
PR 12-FEB-1998; 98US-0022939.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J; Bandman O, Baughn M, Corley NC, Guegler KJ;

(1)

Alignment Hillman 1/2

PI Hillman JL, Lal P, Shah P, Tang YT, Yue H;
XX
DR WPI; 1999-494536/41.
DR P-PSDB; AAY15224.
XX
PT New human receptor proteins, used e.g. to treat, prevent and
PT diagnose gastrointestinal and developmental disorders - and related
PT nucleic acids, vectors, transformed cells, antibodies, agonists and
PT antagonists
XX
PS Claim 11; Page 88; 94pp; English.
XX
CC This is the consensus sequence of the Human receptor protein 3 (HURP-3)
CC derived from the following overlapping and/or extended nucleic acid
CC sequences; Incyte clones 611082 (COLNNOT01), 776770 (COLNNOT05), 904152
CC (COLNNOT07), 908496 (COLNNOT09), and 1866665 (SKINBIT01).
CC HURP-3 is expressed in cancerous, inflamed, fetal/proliferating, and
CC reproductive tissue. HURP-3 therefore appears to have a role in some
CC forms of cancer, autoimmune/inflammatory disorders, reproductive
CC disorders, and developmental disorders.
CC This gives rise to the possibility of using an antagonist or an antibody
CC of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.
XX
SQ Sequence 1317 BP; 375 A; 280 C; 278 G; 384 T; 0 other;

Query Match 100.0%; Score 1317; DB 20; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAGGAACAAAGTAAGTCCATTGATACGTTCTTGCCTATCTCTCCTCCAAATCAATGGGCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAGGAACAAAGTAAGTCCATTGATACGTTCTTGCCTATCTCTCCTCCAAATCAATGGGCA 60

Qy         61 CAAACTGTGGCTGGTCTACCTGTGTGGGTTCTGTTCTCTAGATTGGAGGGATGAAGACAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAACTGTGGCTGGTCTACCTGTGTGGGTTCTGTTCTCTAGATTGGAGGGATGAAGACAA 120

Qy        121 GTTCTTGACTCTATGTTGAGGCCAGTTGAAAAATGAGGGAGAATAAAACCATGAACGAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTCTTGACTCTATGTTGAGGCCAGTTGAAAAATGAGGGAGAATAAAACCATGAACGAAA 180

Qy        181 CAAGAAAGAAACAAAACAGAAGAGGAATGAAAAAGACATAATGATGTCATCCAAGCCAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGAAAGAAACAAAACAGAAGAGGAATGAAAAAGACATAATGATGTCATCCAAGCCAAC 240

Qy        241 AAGCCATGCTGAAGTAAATGAAACCATACCCAACCCTTACCCACCAAGCAGCTTTATGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCATGCTGAAGTAAATGAAACCATACCCAACCCTTACCCACCAAGCAGCTTTATGGC 300

Qy        301 TCCTGGATTTCAACAGCCTCTGGGTTCAATCAACTTAGAAAACCAAGCTCAGGGTGCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTGGATTTCAACAGCCTCTGGGTTCAATCAACTTAGAAAACCAAGCTCAGGGTGCTCA 360

Qy        361 GCGTGCTCAGCCCTACGGCATCACATCTCCGGGAATCTTTGCTAGCAGTCAACCGGGTCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCGTGCTCAGCCCTACGGCATCACATCTCCGGGAATCTTTGCTAGCAGTCAACCGGGTCA 420

Qy        421 AGGAAATATACAAATGATAAATCCAAGTGTGGGAACAGCAGTAATGAACTTTAAAGAAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGAAATATACAAATGATAAATCCAAGTGTGGGAACAGCAGTAATGAACTTTAAAGAAGA 480

Qy        481 AGCAAAGGCACTAGGGGTGATCCAGATCATGGTTGGATTGATGCACATTGGTTTTGGAAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGCAAAGGCACTAGGGGTGATCCAGATCATGGTTGGATTGATGCACATTGGTTTTGGAAT 540

Qy        541 TGTTTTGTGTTTAATATCCTTCTCTTTTAGAGAAGTATTAGGTTTTGCCTCTACTGCTGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTTTTGTGTTTAATATCCTTCTCTTTTAGAGAAGTATTAGGTTTTGCCTCTACTGCTGT 600

Qy        601 TATTGGTGGATACCCATTCTGGGGTGGCCTTTCTTTTATTATCTCTGGCTCTCTCTCTGT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 GTCAGCATCCAAGGAGCTTTCCCGTTGTCTGGTGAAAGGCAGCCTGGGAATGAACATTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCAGCATCCAAGGAGCTTTCCCGTTGTCTGGTGAAAGGCAGCCTGGGAATGAACATTGT 720

Qy        721 TAGTTCTATCTTGGCCTTCATTGGAGTGATTCTGCTGCTGGTGGATATGTGCATCAATGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TAGTTCTATCTTGGCCTTCATTGGAGTGATTCTGCTGCTGGTGGATATGTGCATCAATGG 780

Qy        781 GGTAGCTGGCCAAGACTACTGGGCCGTGCTTTCTGGAAAAGGCATTTCAGCCACGCTGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTAGCTGGCCAAGACTACTGGGCCGTGCTTTCTGGAAAAGGCATTTCAGCCACGCTGAT 840

Qy        841 GATCTTCTCCCTCTTGGAGTTCTTCGTAGCTTGTGCCACAGCCCATTTTGCCAACCAAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GATCTTCTCCCTCTTGGAGTTCTTCGTAGCTTGTGCCACAGCCCATTTTGCCAACCAAGC 900

Qy        901 AAACACCACAACCAATATGTCTGTCCTGGTTATTCCAAATATGTATGAAAGCAACCCTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAACACCACAACCAATATGTCTGTCCTGGTTATTCCAAATATGTATGAAAGCAACCCTGT 960

Qy        961 GACACCAGCGTCTTCTTCAGCTCCTCCCAGATGCAACAACTACTCAGCTAATGCCCCTAA 1020
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Db        961 GACACCAGCGTCTTCTTCAGCTCCTCCCAGATGCAACAACTACTCAGCTAATGCCCCTAA 1020

Qy       1021 ATAGTAAAAGAAAAAGGGGTATCAGTCTAATCTCATGGAGAAAAACTACTTGCAAAAACT 1080
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Db       1021 ATAGTAAAAGAAAAAGGGGTATCAGTCTAATCTCATGGAGAAAAACTACTTGCAAAAACT 1080

Qy       1081 TCTTAAGAAGATGTCTTTTATTGTCTACAATGATTTCTAGTCTTTAAAAACTGTGTTTGA 1140
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Db       1081 TCTTAAGAAGATGTCTTTTATTGTCTACAATGATTTCTAGTCTTTAAAAACTGTGTTTGA 1140

Qy       1141 GATTTGTTTTTAGGTTGGTCGCTAATGATGGCTGTATCTCCCTTCACTGTCTCTTCCTAC 1200
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Db       1141 GATTTGTTTTTAGGTTGGTCGCTAATGATGGCTGTATCTCCCTTCACTGTCTCTTCCTAC 1200

Qy       1201 ATTACCACTACTACATGCTGGCAAAGGTGAAGGATCAGAGGACTGAAAAATGATTCTGCA 1260
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Db       1201 ATTACCACTACTACATGCTGGCAAAGGTGAAGGATCAGAGGACTGAAAAATGATTCTGCA 1260

Qy       1261 ACTCTCTTAAAGTTAGAAATGTTTCTGTTCATATTACTTTTTCCTTAATAAAATGTC 1317
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Db       1261 ACTCTCTTAAAGTTAGAAATGTTTCTGTTCATATTACTTTTTCCTTAATAAAATGTC 1317
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RESULT 2
AAZ95381
ID AAZ95381 standard; DNA; 1141 BP.
XX
AC AAZ95381;
XX
DT 01-JUN-2000 (first entry)
XX
DE Human colon specific gene (CSG) SEQ ID NO:3.
XX
KW Human; colon specific gene; CSG; diagnosis; colon cancer; detection;
KW cytostatic; ds.
XX
OS Homo sapiens.
XX
PN WO200007632-A1.
XX
PD 17-FEB-2000.
XX
PF 20-JUL-1999; 99WO-US16357.
XX
PR 04-AUG-1998; 98US-0095231.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Sun Y, Recipon H, Macina RA;
XX
DR WPI; 2000-205579/18.

(4)

Alignment Bandman 1/2

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 28, 2003, 02:03:25 ; Search time 3016.51 Seconds
(without alignments)
17018.784 Million cell updates/sec

Title: US-09-981-353-47
Perfect score: 1764
Sequence: 1 ctcaggcctgacggtccgag.....tgaaaaaaaaaaaaaaagg 1764

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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12: gb_sy:*
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15: em_ba:*
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18: em_in:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1764	100.0	1764	6	AR113044	AR113044 Sequence
2		1743.2	98.8	1768	9	BC018999	BC018999 Homo sapi
3		1740.2	98.7	1760	9	AK000184	AK000184 Homo sapi
4		1723	97.7	1746	6	AX281695	AX281695 Sequence
5		1360.4	77.1	1362	6	AX301999	AX301999 Sequence
6		993.4	56.3	1758	6	AX305693	AX305693 Sequence
7		993.4	56.3	1758	10	MMASML3A	Y08135 M.musculus
8		856.6	48.6	863	6	AX329813	AX329813 Sequence
9		856.6	48.6	863	6	AX330318	AX330318 Sequence
10		856.6	48.6	863	9	HSASML3A	Y08136 H.sapiens m
11		816.4	46.3	1095	6	AX302000	AX302000 Sequence
12	c	628.2	35.6	181342	2	AC023556	AC023556 Homo sapi
13		553.2	31.4	559	6	AX385445	AX385445 Sequence
14		536.8	30.4	540	6	AX386014	AX386014 Sequence
15	c	252.4	14.3	359	6	AX260953	AX260953 Sequence
16		243.8	13.8	1510	6	AX247505	AX247505 Sequence
17		243.8	13.8	1610	6	AX332610	AX332610 Sequence
18		243.8	13.8	1610	6	AX335855	AX335855 Sequence
19		243.8	13.8	1610	9	HSASML3B	Y08134 H.sapiens m
20		242.6	13.8	1489	6	AX247501	AX247501 Sequence
21		235.4	13.3	1948	10	BC009087	BC009087 Mus muscu
22	c	218.2	12.4	122974	2	AC025114	AC025114 Homo sapi
23	c	218.2	12.4	214308	2	AL732434	AL732434 Homo sapi
24		210	11.9	1566	9	BC014444	BC014444 Homo sapi
25		187.2	10.6	181342	2	AC023556	AC023556 Homo sapi
26		147	8.3	2350	9	AK096144	AK096144 Homo sapi
27	c	144.4	8.2	156	6	AX261402	AX261402 Sequence
28		131.8	7.5	214308	2	AL732434	AL732434 Homo sapi
29		103.2	5.9	145430	2	AL845421	AL845421 Danio rer
30		103.2	5.9	192318	2	AL845339	AL845339 Danio rer
31		73.8	4.2	86827	3	PFMAL3P5	AL034556 Plasmodiu
32	c	70.8	4.0	139111	9	AL158048	AL158048 Human DNA
33	c	70.6	4.0	107289	2	AC116923	AC116923 Dictyoste
34		69.2	3.9	171187	2	AC116960	AC116960 Dictyoste
35	c	67.8	3.8	10213	3	PFU27338	U27338 Plasmodium
36	c	66.4	3.8	11829	3	AE001425	AE001425 Plasmodiu
37	c	66	3.7	110000	2	PFMAL13P2_2	Continuation (3 of
38	c	65.2	3.7	110000	2	PFMAL13P2_1	Continuation (2 of
39	c	65	3.7	113117	9	AL512288	AL512288 Human DNA
40		64.8	3.7	14867	3	AE001398	AE001398 Plasmodiu
41	c	64.8	3.7	92633	2	PFMAL4P1_3	Continuation (4 of
42	c	64.8	3.7	106434	3	AC117080	AC117080 Dictyoste
43		64.4	3.7	14551	6	AX281473	AX281473 Sequence
44		64	3.6	29016	2	AC117266	AC117266 Dictyoste
45	c	63.8	3.6	92376	8	AC006282	AC006282 Arabidops

ALIGNMENTS

RESULT 1
AR113044
LOCUS AR113044 1764 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 13 from patent US 6132964.
ACCESSION AR113044
VERSION AR113044.1 GI:14093366
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1764)
AUTHORS Bandman,O., Lal,P., Hillman,J.L., Corley,N.C., Guegler,K.J. and Shah,P.
TITLE Hydrolase enzymes
JOURNAL Patent: US 6132964-A 13 17-OCT-2000;

4

Alignment Bandman 7c

FEATURES Location/Qualifiers
source 1. .1764
/organism="unknown"
BASE COUNT 537 a 356 c 344 g 527 t
ORIGIN

Query Match 100.0%; Score 1764; DB 6; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTCAGGCCTGACGGTCCGAGTGGAGCTGCGGGACAGCCCGAACCTCCAGGTCAGCCCCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGCCTGACGGTCCGAGTGGAGCTGCGGGACAGCCCGAACCTCCAGGTCAGCCCCGC 60

Qy         61 GGCCCTCCATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCTCCATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCC 120

Qy        121 GCTCCGGCCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAG 180
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Db        121 GCTCCGGCCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAG 180

Qy        181 GACAGTTTTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACC 240
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Db        181 GACAGTTTTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACC 240

Qy        241 ACACAAAAGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAG 300
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Db        241 ACACAAAAGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAG 300

Qy        301 ATGTTCTGTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATT 360
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Db        301 ATGTTCTGTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATT 360

Qy        361 CTGGACAAGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTAC 420
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Db        361 CTGGACAAGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTAC 420

Qy        421 CTGAACTCTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGA 480
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Db        421 CTGAACTCTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGA 480

Qy        481 GTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGG 540
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Db        481 GTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGG 540

Qy        541 ATCAACTGCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCAT 600
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Db        541 ATCAACTGCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCAT 600

Qy        601 GGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTA 660
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Db        601 GGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTA 660

Qy        661 CAACTAATCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATA 720
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Db        661 CAACTAATCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATA 720

Qy        721 TAATGACACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGA 780
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Db        721 TAATGACACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGA 780

Qy        781 ACAACTCTCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATC 840
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Db        781 ACAACTCTCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATC 840

Qy        841 TGCCATCTTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATA 900
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Db        841 TGCCATCTTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATA 900

Qy        901 TTTTTCAAAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACA 960
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Db        901 TTTTTCAAAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACA 960

Qy        961 GCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTG 1020
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Db        961 GCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTG 1020

Qy       1021 CTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGT 1080

Qy       1081 TTCAGTATGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGA 1140
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Db       1081 TTCAGTATGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGA 1140

Qy       1141 CAGAGGCGAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCT 1200
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Db       1141 CAGAGGCGAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCT 1200

Qy       1201 ACGACATTGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCC 1260
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Db       1201 ACGACATTGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCC 1260

Qy       1261 TAGACAGTAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTG 1320
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Db       1261 TAGACAGTAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTG 1320

Qy       1321 TAACATGTGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATA 1380
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Db       1321 TAACATGTGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATA 1380

Qy       1381 TTTCCTATGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAGTATTTCACAG 1440
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Qy       1501 AATCTTTGTTAATTACTGAGTGGGCAAGTAGACTTCCTGTCTTTGCTTTCTTTTTTTTTT 1560
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Qy       1741 AATATGAAAAAAAAAAAAAAAAGG 1764
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Db       1741 AATATGAAAAAAAAAAAAAAAAGG 1764
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RESULT 2
BC018999
LOCUS BC018999 1768 bp mRNA linear PRI 11-DEC-2001
DEFINITION Homo sapiens, clone MGC:20681 IMAGE:3138813, mRNA, complete cds.
ACCESSION BC018999
VERSION BC018999.1 GI:17512052
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian

Alignment Gunn 1/3

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Db       2543 TACTTGTGCTATAACTGCTTTTGTGCTAAATATGAATTGTCTCAAAATTAGCTGTGTAAA 2602

Qy       2677 ATAGCCCGGGTTCCACTGGCTCCTGCTGAGGTCCCCTTTCCTTCTGGGCTGTGAATTCCT 2736
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Db       2603 ATAGCCCGGGTTCCACTGGCTCCTGCTGAGGTCCCCTTTCCTTCTGGGCTGTGAATTCCT 2662

Qy       2737 GTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCCATTATGTTTTAATGTTGTCTC 2796
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Db       2663 GTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCCATTATGTTTTAATGTTGTCTC 2722

Qy       2797 TGAAGATGACTTGTGATTTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACAGAG 2856
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Db       2723 TGAAGATGACTTGTGATTTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACAGAG 2782

Qy       2857 CATGCTCTGCGTTGTTGGTTTCACCAGCTTCTGCCCTCACATGCACAGGGATTTAACAAC 2916
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Qy       2977 CCCTCCTGTCAGTAGTGGCAGGATCTATTGGCATATTCGGGAGCTTCTTAGAGGGATGAG 3036
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Qy       3037 GTTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTGCAAGCAGTTTATTGACTG 3096
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Qy       3097 TTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTTTAA 3156
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Db       3023 TTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTTTAA 3082

Qy       3157 GATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAAAT 3216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3083 GATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAAAT 3142

Qy       3217 GGGACAGCCTTCCATGTTCATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTT 3276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3143 GGGACAGCCTTCCATGTTCATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTT 3202

Qy       3277 TAGAAAAAA 3285
             |||||||||
Db       3203 TAGAAAAAA 3211
```

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RESULT 6
AAV33501
ID   AAV33501 standard; cDNA; 3220 BP.
XX
AC   AAV33501;
XX
DT   18-JAN-1999  (first entry)
XX
DE   Human sodium-lithium countertransporter hPiT-1 cDNA.
XX
KW   Sodium-lithium countertransporter; sodium-phosphate cotransporter;
KW   PiT-1; human; leukaemia virus receptor 1; lithium therapy;
KW   manic depression; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             371..2410
FT                   /*tag= a
FT                   /product= leukaemia virus receptor 1
XX
PN   WO9838203-A1.
XX
PD   03-SEP-1998.
XX
PF   11-FEB-1998;   98WO-US02875.
XX
PR   27-FEB-1997;   97US-0039462.
XX
PA   (UYEM-) UNIV EMORY.
XX
PI   Gunn RB,  Timmer RT;
XX
DR   WPI; 1998-520759/44.
DR   P-PSDB; AAW70498.
XX
PT   New isolated lithium-sodium counter-transporter DNA - used to
PT   develop products for evaluating lithium-sodium transport in
PT   erythrocytes, particularly for lithium therapy in manic depression.
XX
PS   Claim 3; Page 35-37; 64pp; English.
XX
CC   This DNA molecule encodes human lithium-sodium countertransporter
CC   (LSCT) PiT-1 (see AAW70498).  Human PiT-1 is also a sodium-phosphate
CC   cotransporter and a human amphotrophic retrovirus receptor
CC   (leukaemia virus receptor 1).  LSCTs such as PiT-1 provide the
CC   physiological mechanism for the extrusion of lithium from cells,
CC   i.e. it regulates the cell concentration of lithium.  Its activity
CC   determines the therapeutic effect of lithium.  The invention
CC   provides a simple molecular biological test for the ability of
CC   cells to extrude lithium.  The LSCTs have signficance for
CC   determining the responsiveness of humans with mental disorders,
CC   including manic depressives, to treatment with lithium salts.
CC   Probes and primers for PiT-1, PiT-2 (see AAV33502) and BNPI (see
CC   AAV33503) can be used in diagnostic tests useful for genetic
CC   screenings to predict whether a patient will respond to lithium
CC   treatment.  The test is also a screen for susceptibility to, and
CC   extent of, manic depressive illness, and is suitable for screening
CC   newborns.
XX
SQ   Sequence 3220 BP; 784 A; 710 C; 762 G; 964 T; 0 other;
```

Query Match 96.5%; Score 3173.6; DB 19; Length 3220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3181; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
Qy         97 CCGACCCGGGCCGTGTGCCCGTGGCTCCAGCCGCTGCCGCCTCGATCTCCTCGTCTCCCG 156
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 CCGGGCCGTGCCGTGTGCCCGTGGCTCCAGCCGCTGCCGCCTCGATCTCCTCGTCTCCCG 83

Qy        157 CTCCGCCCTCCCTTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTC 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTCCGCCCTCCCTTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTC 143

Qy        217 TGCTCCGTGCTTTTAGCCCTCCTGAGCCAAAGAAACCCCAGACAACAGATGCCCATACGC 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCTCCGTGCTTTTAGCCCTCCTGAGCCAAAGAAACCCCAGACAACAGATGCCCATACGC 203

Qy        277 AGCGTATAGCAGTAACTCCCCAGCTCGGTTTCTGTGCCGTAGTTTACAGTATTTAATTTT 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCGTATAGCAGTAACTCCCCAGCTCGGTTTCTGTGCCGTAGTTTACAGTATTTAATTTT 263

Qy        337 ATATAATATATATTATTTATTATAGCATTTTTGATACCTCATATTCTGTTTACACATCTT 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 ATATAATATATATTATTTATTATAGCATTTTTGATACCTCATATTCTGTTTACACATCTT 323

Qy        397 GAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGAATGGCAACGGTGA 456
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        324 GAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGAATGGCAACGCTGA 383

Qy        457 TTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGC 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGC 443

Qy        517 TCATCCTGGGCTTCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TCATCCTGGGCTTCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAG 503

Qy        577 CAAATTCTTTTGGTACAGCTGTGGGCTCAGGTGTAGTGACCCTGAAGCAAGCCTGCATCC 636
```

(9)

Alignment Gunn 3/3

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Db        504 CAAATTCTTTTGGTACAGCTGTGGGCTCAGGTGTAGTGACCCTAAAGCAAGCCTGCATCC 563
Qy        637 TAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGGCCAAAGTGAGCGAAACCA 696
Db        564 TAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGGCCAAAGTGAGCGAAACCA 623
Qy        697 TCCGGAAGGGCTTGATTGACGTGGAGATGTACAACTCGACTCAAGGGCTACTGATGGCCG 756
Db        624 TCCGGAAGGGCTTGATTGACGTGGAGATGTACAACTCGACTCAAGGGCTACTGATGGCCG 683
Qy        757 GCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGC 816
Db        684 GCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGC 743
Qy        817 TCCCTATTTCTGGAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAA 876
Db        744 TCCCTATTTCTGGAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAA 803
Qy        877 AGGGGCAGGAGGGTGTCAAGTGGTCTGAACTGATAAAAATTGTGATGTCTTGGTTCGTGT 936
Db        804 AGGGGCAGGAGGGTGTCAAGTGGTCTGAACTGATAAAAATTGTGATGTCTTGGTTCGTGT 863
Qy        937 CCCCACTGCTTTCTGGAATTATGTCTGGAATTTTATTCTTCCTGGTTCGTGCATTCATCC 996
Db        864 CCCCACTGCTTTCTGGAATTATGTCTGGAATTTTATTCTTCCTGGTTCGTGCATTCATCC 923
Qy        997 TCCATAAGGCAGATCCAGTTCCTAATGGTTTGCGAGCTTTGCCAGTTTTCTATGCCTGCA 1056
Db        924 TCCATAAGGCAGATCCAGTTCCTAATGGTTTGCGAGCTTTGCCAGTTTTCTATGCCTGCA 983
Qy       1057 CAGTTGGAATAAACCTCTTTTCCATCATGTATACTGGAGCACCGTTGCTGGGCTTTGACA 1116
Db        984 CAGTTGGAATAAACCTCTTTTCCATCATGTATACTGGAGCACCGTTGCTGGGCTTTGACA 1043
Qy       1117 AACTTCCTCTGTGGGGTACCATCCTCATCTCGGTGGGATGTGCAGTTTTCTGTGCCCTTA 1176
Db       1044 AACTTCCTCTGTGGGGTACCATCCTCATCTCGGTGGGATGTGCAGTTTTCTGTGCCCTTA 1103
Qy       1177 TCGTCTGGTTCTTTGTATGTCCCAGGATGAAGAGAAAAATTGAACGAGAAATAAAGTGTA 1236
Db       1104 TCGTCTGGTTCTTTGTATGTCCCAGGATGAAGAGAAAAATTGAACGAGAAATAAAGTGTA 1163
Qy       1237 GTCCTTCTGAAAGCCCCTTAATGGAAAAAAAGAATAGCTTGAAAGAAGACCATGAAGAAA 1296
Db       1164 GTCCTTCTGAAAGCCCCTTAATGGAAAAAAAGAATAGCTTGAAAGAAGACCATGAAGAAA 1223
Qy       1297 CAAAGTTGTCTGTTGGTGATATTGAAAACAAGCATCCTGTTTCTGAGGTAGGGCCTGCCA 1356
Db       1224 CAAAGTTGTCTGTTGGTGATATTGAAAACAAGCATCCTGTTTCTGAGGTAGGGCCTGCCA 1283
Qy       1357 CTGTGCCCCTCCAGGCTGTGGTGGAGGAGAGAACAGTCTCATTCAAACTTGGAGATTTGG 1416
Db       1284 CTGTGCCCCTCCAGGCTGTGGTGGAGGAGAGAACAGTCTCATTCAAACTTGGAGATTTGG 1343
Qy       1417 AGGAAGCTCCAGAGAGAGAGAGGCTTCCCAGCGTGGACTTGAAAGAGGAAACCAGCATAG 1476
Db       1344 AGGAAGCTCCAGAGAGAGAGAGGCTTCCCAGCGTGGACTTGAAAGAGGAAACCAGCATAG 1403
Qy       1477 ATAGCACCGTGAATGGTGCAGTGCAGTTGCCTAATGGGAACCTTGTCCAGTTCAGTCAAG 1536
Db       1404 ATAGCACCGTGAATGGTGCAGTGCAGTTGCCTAATGGGAACCTTGTCCAGTTCAGTCAAG 1463
Qy       1537 CCGTCAGCAACCAAATAAACTCCAGTGGCCACTACCAGTATCACACCGTGCATAAGGATT 1596
Db       1464 CCGTCAGCAACCAAATAAACTCCAGTGGCCACTCCCAGTATCACACCGTGCATAAGGATT 1523
Qy       1597 CCGGCCTGTACAAAGAGCTACTCCATAAATTACATCTTGCCAAGGTGGGAGATTGCATGG 1656
Db       1524 CCGGCCTGTACAAAGAGCTACTCCATAAATTACATCTTGCCAAGGTGGGAGATTGCATGG 1583
Qy       1657 GAGACTCCGGTGACAAACCCTTAAGGCGCAATAATAGCTATACTTCCTATACCATGGCAA 1716
Db       1584 GAGACTCCGGTGACAAACCCTTAAGGCGCAATAATAGCTATACTTCCTATACCATGGCAA 1643
Qy       1717 TATGTGGCATGCCTCTGGATTCATTCCGTGCCAAAGAAGGTGAACAGAAGGGCGAAGAAA 1776
Db       1644 TATGTGGCATGCCTCTGGATTCATTCCGTGCCAAAGAAGGTGAACAGAAGGGCGAAGAAA 1703
Qy       1777 TGGAGAAGCTGACATGGCCTAATGCAGACTCCAAGAAGCGAATTCGAATGGACAGTTACA 1836
Db       1704 TGGAGAAGCTGACATGGCCTAATGCAGACTCCAAGAAGCGAATTCGAATGGACAGTTACA 1763
Qy       1837 CCAGTTACTGCAATGCTGTGTCTGACCTTCACTCAGCATCTGAGATAGACATGAGTGTCA 1896
Db       1764 CCAGTTACTGCAATGCTGTGTCTGACCTTCACTCAGCATCTGAGATAGACATGAGTGTCA 1823
Qy       1897 AGGCAGAGATGGGTCTAGGTGACAGAAAAGGAAGTAATGGCTCTCTAGAAGAATGGTATG 1956
Db       1824 AGGCAGCGATGGGTCTAGGTGACAGAAAAGGAAGTAATGGCTCTCTAGAAGAATGGTATG 1883
Qy       1957 ACCAGGATAAGCCTGAAGTCTCTCTCCTCTTCCAGTTCCTGCAGATCCTTACAGCCTGCT 2016
Db       1884 ACCAGGATAAGCCTGAAGTCTCTCTCCTCTTCCAGTTCCTGCAGATCCTTACAGCCTGCT 1943
Qy       2017 TTGGGTCATTCGCCCATGGTGGCAATGACGTAAGCAATGCCATTGGGCCTCTGGTTGCTT 2076
Db       1944 TTGGGTCATTCGCCCATGGTGGCAATGACGTAAGCAATGCCATTGGGCCTCTGGTTGCTT 2003
Qy       2077 TATATTTGGTTTATGACACAGGAGATGTTTCTTCAAAAGTGGCAACACCAATATGGCTTC 2136
Db       2004 TATATTTGGTTTATGACACAGGAGATGTTTCTTCAAAAGTGGCAACACCAATATGGCTTC 2063
Qy       2137 TACTCTATGGTGGTGTTGGTATCTGTGTTGGTCTGTGGGTTTGGGGAAGAAGAGTTATCC 2196
Db       2064 TACTCTATGGTGGTGTTGGTATCTGTGTTGGTCTGTGGGTTTGGGGAAGAAGAGTTATCC 2123
Qy       2197 AGACCATGGGGAAGGATCTGACACCGATCACACCCTCTAGTGGCTTCAGTATTGAACTGG 2256
Db       2124 AGACCATGGGGAAGGATCTGACACCGATCACACCCTCTAGTGGCTTCAGTATTGAACTGG 2183
Qy       2257 CATCTGCCCTCACTGTGGTGATTGCATCAAATATTGGCCTTCCCATCAGTACAACACATT 2316
Db       2184 CATCTGCCCTCACTGTGGTGATTGCATCAAATATTGGCCTTCCCATCAGTACAACACATT 2243
Qy       2317 GTAAAGTGGGCTCTGTTGTGTCTGTTGGCTGGCTCCGGTCCAAGAAGGCTGTTGACTGGC 2376
Db       2244 GTAAAGTGGGCTCTGTTGTGTCTGTTGGCTGGCTCCGGTCCAAGAAGGCTGTTGACTGGC 2303
Qy       2377 GTCTCTTTCGTAACATTTTTATGGCCTGGTTTGTCACAGTCCCCATTTCTGGAGTTATCA 2436
Db       2304 GTCTCTTTCGTAACATTTTTATGGCCTGGTTTGTCACAGTCCCCATTTCTGGAGTTATCA 2363
Qy       2437 GTGCTGCCATCATGGCAATCTTCAGATATGTCATCCTCAGAATGTGAAGCTGTTTGAGAT 2496
Db       2364 GTGCTGCCATCATGGCAATCTTCAGATATGTCATCCTCAGAATGTGAAGCTGTTTGAGAT 2423
Qy       2497 TAAAATTTGTGTCAATGTTTGGGACCATCTTAGGTATTCCTGCTCCCCTGAAGAATGATT 2556
Db       2424 TAAAATTTGTGTCAATGTTTGGGACCATCTTAGGTATTCCTGCTCCCCTGAAGAATGATT 2483
Qy       2557 ACAGTGTTAACAGAAGACTGACAAGAGTCTTTTTATTTGGGAGCCAGAGGAGGGAAGTGT 2616
Db       2484 ACAGTGTTAACAGAAGACTGACAAGAGTCTTTTTATTTGGGAG-CAGAGGAGGGAAGTGT 2542
Qy       2617 TACTTGTGCTATAACTGCTTTTGTGCTAAATATGAATTGTCTCAAAATTAGCTGTGTAAA 2676
Db       2543 TACTTGTGCTATAACTGCTTTTGTGCTAAATATGAATTGTCTCAAAATTAGCTGTGTAAA 2602
Qy       2677 ATAGCCCGGGTTCCACTGGCTCCTGCTGAGGTCCCCTTTCCTTCTGGGCTGTGAATTCCT 2736
Db       2603 ATAGCCCGGGTTCCACTGGCTCCTGCTGAGGTCCCCTTTCCTTCTGGGCTGTGAATTCCT 2662
Qy       2737 GTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCCATTATGTTTTAATGTTGTCTC 2796
Db       2663 GTACATATTTCTCTACTTTTTGTATCAGGCTTCAATTCCATTATGTTTTAATGTTGTCTC 2722
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Alignment Gaps 3/3

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Qy       2797 TGAAGATGACTTGTGATTTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACAGAG 2856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2723 TGAAGATGACTTGTGATTTTTTTTTCTTTTTTTTAAACCATGAAGAGCCGTTTGACAGAG 2782

Qy       2857 CATGCTCTGCGTTGTTGGTTTCACCAGCTTCTGCCCTCACATGCACAGGGATTTAACAAC 2916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2783 CATGCTCTGCGTTGTTGGTTTCACCAGCTTCTGCCCTCACATGCACAGGGATTTAACAAC 2842

Qy       2917 AAAAATATAACTACAACTTCCCTTGTAGTCTCTTATATAAGTAGAGTCCTTGGTACTCTG 2976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2843 AAAAATATAACTACAACTTCCCTTGTAGTCTCTTATATAAGTAGAGTCCTTGGTACTCTG 2902

Qy       2977 CCCTCCTGTCAGTAGTGGCAGGATCTATTGGCATATTCGGGAGCTTCTTAGAGGGATGAG 3036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2903 CCCTCCTGTCAGTAGTGGCAGGATCTATTGGCATATTCGGGAGCTTCTTAGAGGGATGAG 2962

Qy       3037 GTTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTGCAAGCAGTTTATTGACTG 3096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2963 GTTCTTTGAACACAGTGAAAATTTAAATTAGTAACTTTTTTGCAAGCAGTTTATTGACTG 3022

Qy       3097 TTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTTTAA 3156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3023 TTATTGCTAAGAAGAAGTAAGAAAGAAAAAGCCTGTTGGCAATCTTGGTTATTTCTTTAA 3082

Qy       3157 GATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAAAT 3216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3083 GATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAAAT 3142

Qy       3217 GGGACAGCCTTCCATGTTCATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTT 3276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3143 GGGACAGCCTTCCATGTTCATTTGTCTACCTCTTAACTGAATAAAAAAGCCTACAGTTTT 3202

Qy       3277 TAGAAAAAA 3285
             |||||||||
Db       3203 TAGAAAAAA 3211
```

RESULT 7
AAQ10676
ID AAQ10676 standard; DNA; 3211 BP.
XX
AC AAQ10676;
XX
DT 26-APR-1991 (first entry)
XX
DE Human gibbon ape leukaemia virus receptor gene.
XX
KW Human gibbon ape leukaemia virus receptor; GALV; retroviruses; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   371..2410
FT   /*tag= a
FT   /product= Human GALV receptor protein
XX
PN EP414035-A.
XX
PD 27-FEB-1989.
XX
PF 14-AUG-1990; 90EP-0115136.
XX
PR 24-AUG-1989; 89US-0398351.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI O'Hara BM;
XX
DR WPI; 1991-059307/09.
DR P-PSDB; AAR10848.
XX
PT - capable of regulating viral entry into cells
XX
PS Disclosure; page 8; 26pp; English.
XX
CC This human gibbon ape leukaemia virus (GALV) receptor gene encodes
CC a GALV receptor protein required for the entry of the virus into
CC cells. Manipulation of the receptor sequence could therefore result
CC in regulation of retroviral infection of cells. This gene and the
CC protein prod. are useful in analysis of virus/receptor interaction.
XX
SQ Sequence 3211 BP; 781 A; 708 C; 760 G; 962 T; 0 other;

Query Match 96.4%; Score 3172; DB 12; Length 3211;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3180; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy         97 CCGACCCGGGCCGTGTGCCCGTGGCTCCAGCCGCTGCCGCCTCGATCTCCTCGTCTCCCG 156
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 CCGGGCCGTGCCGTGTGCCCGTGGCTCCAGCCGCTGCCGCCTCGATCTCCTCGTCTCCCG 83

Qy        157 CTCCGCCCTCCCTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTC 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTCCGCCCTCCCTTTCCCTGGATGAACTTGCGTCCTTTCTCTTCTCCGCCATGGAATTC 143

Qy        217 TGCTCCGTGCTTTTAGCCCTCCTGAGCCAAAGAAACCCCAGACAACAGATGCCCATACGC 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCTCCGTGCTTTTAGCCCTCCTGAGCCAAAGAAACCCCAGACAACAGATGCCCATACGC 203

Qy        277 AGCGTATAGCAGTAACTCCCCAGCTCGGTTTCTGTGCCGTAGTTTACAGTATTTAATTTT 336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCGTATAGCAGTAACTCCCCAGCTCGGTTTCTGTGCCGTAGTTTACAGTATTTAATTTT 263

Qy        337 ATATAATATATATTATTTATTATAGCATTTTTGATACCTCATATTCTGTTTACACATCTT 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 ATATAATATATATTATTTATTATAGCATTTTTGATACCTCATATTCTGTTTACACATCTT 323

Qy        397 GAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGAATGGCAACGGTGA 456
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        324 GAAAGGCGCTCAGTAGTTCTCTTACTAAACAACCACTACTCCAGAGAATGGCAACGCTGA 383

Qy        457 TTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGC 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TTACCAGTACTACAGCTGCTACCGCCGCTTCTGGTCCTTTGGTGGACTACCTATGGATGC 443

Qy        517 TCATCCTGGGCTTCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TCATCCTGGGCTTCATTATTGCATTTGTCTTGGCATTCTCCGTGGGAGCCAATGATGTAG 503

Qy        577 CAAATTCTTTTGGTACAGCTGTGGGCTCAGGTGTAGTGACCCTGAAGCAAGCCTGCATCC 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CAAATTCTTTTGGTACAGCTGTGGGCTCAGGTGTAGTGACCCTGAAGCAAGCCTGCATCC 563

Qy        637 TAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGGCCAAAGTGAGCGAAACCA 696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 TAGCTAGCATCTTTGAAACAGTGGGCTCTGTCTTACTGGGGGCCAAAGTGAGCGAAACCA 623

Qy        697 TCCGGAAGGGCTTGATTGACGTGGAGATGTACAACTCGACTCAAGGGCTACTGATGGCCG 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 TCCGGAAGGGCTTGATTGACGTGGAGATGTACAACTCGACTCAAGGGCTACTGATGGCCG 683

Qy        757 GCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGC 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 GCTCAGTCAGTGCTATGTTTGGTTCTGCTGTGTGGCAACTCGTGGCTTCGTTTTTGAAGC 743

Qy        817 TCCCTATTTCTGGAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAA 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 TCCCTATTTCTGGAACCCATTGTATTGTTGGTGCAACTATTGGTTTCTCCCTCGTGGCAA 803

Qy        877 AGGGGCAGGAGGGTGTCAAGTGGTCTGAACTGATAAAAATTGTGATGTCTTGGTTCGTGT 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 AGGGGCAGGAGGGTGTCAAGTGGTCTGAACTGATAAAAATTGTGATGTCTTGGTTCGTGT 863

Qy        937 CCCCACTGCTTTCTGGAATTATGTCTGGAATTTTATTCTTCCTGGTTCGTGCATTCATCC 996
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[redacted]ibbon ape leukaemia virus receptor isolated from different sources